

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 15, 2003, 16:58:02 ; Search time 1852.4 Seconds
(without alignments)
122 402 Million cell updates/sec

Title: US-09-856-070-17
Perfect score: 69
Sequence: 1 EREKFMMEKEEL 14

Scoring table. H2OSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Del-ext 7.0

Searched: 16154066 seqs, 8037743376 residues

Total number of hits satisfying chosen parameters: 32308142

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame_plus_p2n model -DEV-xip
-Q/cq/2.1/USP-0.5p2n/US09856070/frameset/140129001558341644/app-query fasta_1 1592
-DB=EST -QEMT=fastap -SUFFIX=rsr -MINMATCH=0.1 -LAP-PL=0 -LAPPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40 codi -LIST=45
-DOALIGN=206 -THE_SCORE=opt -THP_MAX=100 -THP_MIN=0 -ALIGN 15 -MODE=DUAL
-OUTFM=ptc -NORM=ext -HAPSIZE=530 -MINLEN=0 -MAXLEN=200000000
-USER=US09856070-3322-07.dat_14012903_155834_1644 -NCPU=6 -ICPU=4
-NO_XIPXY -NO_WMAP -LAPQUERY -NC_STOPS=0 -WAIT -LONGMAP -DEV-IMP000-120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -PGAP=10 -PGAPEXT=7
-XGAPOP=10 -YGAPEXT=0.5 -DELCP=6 -DELEXT=7

Database: EST *

- 1: em_estbta: *
- 2: em_estlun: *
- 3: em_estlin: *
- 4: em_estimu: *
- 5: em_estlov: *
- 6: em_estpli: *
- 7: em_estro: *
- 8: em_hic: *
- 9: qb_estl1: *
- 10: qb_estl2: *
- 11: qb_hic: *
- 12: qb_est3: *
- 13: qb_est4: *
- 14: qb_est5: *
- 15: em_estlun: *
- 16: em_estrom: *
- 17: qb_ess: *
- 18: em_ess_hum: *
- 19: em_ess_fov: *
- 20: em_ess_plin: *
- 21: em_ess_vrt: *
- 22: em_ess_fun: *
- 23: em_ess_mam: *
- 24: em_ess_mus: *
- 25: em_ess_other: *
- 26: em_ess_pro: *
- 27: em_ess_rod: *

Prd. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	69	100.0	214	13	R1052878
2	69	100.0	214	14	R1054475
3	69	100.0	215	14	RQ467435
4	69	100.0	234	12	RQ467435
5	69	100.0	245	12	BP443034
6	69	100.0	275	14	BM844124
7	69	100.0	279	12	BP443034
8	69	100.0	281	10	AW455219
9	69	100.0	294	13	R1050028
10	69	100.0	312	14	RQ467435
11	69	100.0	335	9	AW455219
12	69	100.0	358	14	RQ467435
13	69	100.0	364	14	RQ467435
14	69	100.0	401	14	RQ467435
15	69	100.0	404	14	BM744771
16	69	100.0	413	14	BQ467435
17	69	100.0	432	12	BP443034
18	69	100.0	437	14	BM844124
19	69	100.0	447	10	AW455219
20	69	100.0	455	14	BM844124
21	69	100.0	460	14	BM844124
22	69	100.0	469	9	AW455219
23	69	100.0	484	10	AW455219
24	69	100.0	484	10	BE314916
25	69	100.0	484	14	BM844124
26	69	100.0	499	14	R1054475
27	69	100.0	496	14	BM785233
28	69	100.0	507	14	BM844124
29	69	100.0	543	10	AW455219
30	69	100.0	543	9	AW455219
31	69	100.0	543	14	BM785233
32	69	100.0	543	14	BM785233
33	69	100.0	548	14	BM785233
34	69	100.0	553	14	BM785233
35	69	100.0	558	12	BP443034
36	69	100.0	564	12	BP443034
37	69	100.0	574	14	BM744665
38	69	100.0	574	10	BP443034
39	69	100.0	583	14	BM785233
40	69	100.0	590	14	BM785233
41	69	100.0	592	14	BM740878
42	69	100.0	593	14	BM785233
43	69	100.0	605	10	BE177808
44	69	100.0	605	13	BE177808
45	69	100.0	615	14	BM785233

ALIGNMENTS

RESULT 1
BI052878
LOCUS R1052878 214 bp mRNA linear EST 15-JUN-2001
DEFINITION R1052878 Homo sapiens cDNA, mRNA sequence.
ACCESSION BI052878
VERSION BI052878.1 GI:14456408
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 214)
Dias Neto, E., Garcia Correa, P., Veljovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Raia, G.S., Simpson, D.H.,

Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hale
M.J., Soares, F., Brontani, R.P., Reis, J.F., de Souza, S.J. and
Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663

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This sequence was derived from the FAFESP/11CR Human Cancer Genome Project. This entry can be seen in the following URL (<http://www.ludwig.org.br/scripts/getitem2.pl?PI=PC562-WC5-CN02a1-200101-021-F0242-2001-WC3644-1>)

Accession BM27086
Version BM27086.1 GI:1918495
Keywords EST.
Source Human.

Organism Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

Reference 1 (bases 1 to 312)
Dias Neto, F., Garcia Corrojo, A., Verjovsky-Almeida, S., Brites, M.R.,
Nagai, M.A., da Silva, W. Jr., Zazo, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Balda, G.S., Simpson, D.H.,
Brunslein, A., de Oliveira, P.S., Bucher, P., Jonkeel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.P., Reis, J.F., de Souza, S.J., and
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Authors Shogun sequencing of the human transcriptome with ORF expressed
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Title Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

Journal MEDLINE 20202663
Comment Contact: Simpson A.J.O.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Genome Project.
This entry can be seen in the following URL
(http://www.ludwig.org.br/seq/gethtml.pl?1-QV612-QV-BT223-036.html
&13-220499614-1)

Features Seq primer: puc 18 forward.
location/Qualifiers
1..335
/oranism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="BT223"
/tissue_type="Adult"
/note="Organ: breast; Vector: puc18; Site: 1; Small: Site_2;
Small: A mini-library was made by cloning products derived
from OPSTES PCR (U.S. Letters Patent application No. 196
716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

Base Count 103 a 65 c 128 q 39 t
Origin

Alignment Scores:
Pred. No.: 0.186 Length: 345
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-856-070-17 (1-14) x AI909763 (1-312)

QY 1 GluArqGluLysGluMetMetArqGluLysGluLeu 14
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143 GAGACACAAAGATAGCAGATCATCTGTGCAGACAGCACTTG 184

RESULT 12
BQ323837
LOCUS BQ323837 358 bp mRNA linear EST 17 MAY 2002
DEFINITION CMO-C10095-301000-648-b05 Homo sapiens cDNA, mRNA sequence.
ACCESSION BQ323837
VERSION BQ323837.1 GI:20935634
KEYWORDS EST.
SOURCE Human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

Reference: 1 (bases 1 to 358)
Dias Neto, F., Garcia Corrojo, A., Verjovsky-Almeida, S., Brites, M.R.,
Nagai, M.A., da Silva, W. Jr., Zazo, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Balda, G.S., Simpson, D.H.,
Brunslein, A., de Oliveira, P.S., Bucher, P., Jonkeel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.P., Reis, J.F., de Souza, S.J., and
Simpson, A.J.

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Journal MEDLINE 20202663
Comment Contact: Simpson A.J.O.
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Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Genome Project.
This entry can be seen in the following URL
(http://www.ludwig.org.br/seq/gethtml.pl?1-QV612-QV-BT223-036.html
&13-220499614-1)

Features Seq primer: puc 18 forward.
location/Qualifiers
1..335
/oranism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="BT223"
/tissue_type="Adult"
/note="Organ: breast; Vector: puc18; Site: 1; Small: Site_2;
Small: A mini-library was made by cloning products derived
from OPSTES PCR (U.S. Letters Patent application No. 196
716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

Base Count 108 a 60 c 110 q 34 t
Origin

Alignment Scores:
Pred. No.: 0.174 Length: 312
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-09-856-070-17 (1-14) x BM27086 (1-312)

QY 1 GluArqGluLysGluMetMetArqGluLysGluLeu 14
|||||
182 GAGACACAAAGATAGCAGATCATCTGTGCAGACAGCACTTG 223

RESULT 11
LOCUS AI909763
DEFINITION QV-BT223-220499-036-BT223 Homo sapiens cDNA, mRNA sequence.
ACCESSION AI909763
VERSION AI909763.1 GI:6500444
KEYWORDS EST.
SOURCE Human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

Reference: 1 (bases 1 to 312)
Dias Neto, F., Garcia Corrojo, A., Verjovsky-Almeida, S., Brites, M.R.,
Nagai, M.A., da Silva, W. Jr., Zazo, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Balda, G.S., Simpson, D.H.,
Brunslein, A., de Oliveira, P.S., Bucher, P., Jonkeel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.P., Reis, J.F., de Souza, S.J., and
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Ludwig Institute for Cancer Research
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Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Genome Project.
This entry can be seen in the following URL
(http://www.ludwig.org.br/seq/gethtml.pl?1-QV612-QV-BT223-036.html
&13-220499614-1)

Features Seq primer: puc 18 forward.
location/Qualifiers
1..335
/oranism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="BT223"
/tissue_type="Adult"
/note="Organ: breast; Vector: puc18; Site: 1; Small: Site_2;
Small: A mini-library was made by cloning products derived
from OPSTES PCR (U.S. Letters Patent application No. 196
716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

Base Count 108 a 60 c 110 q 34 t
Origin

Alignment Scores:
Pred. No.: 0.174 Length: 312
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-09-856-070-17 (1-14) x BM27086 (1-312)

QY 1 GluArqGluLysGluMetMetArqGluLysGluLeu 14
|||||
182 GAGACACAAAGATAGCAGATCATCTGTGCAGACAGCACTTG 223

RESULT 11
LOCUS AI909763
DEFINITION QV-BT223-220499-036-BT223 Homo sapiens cDNA, mRNA sequence.
ACCESSION AI909763
VERSION AI909763.1 GI:6500444
KEYWORDS EST.
SOURCE Human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

Reference: 1 (bases 1 to 312)
Dias Neto, F., Garcia Corrojo, A., Verjovsky-Almeida, S., Brites, M.R.,
Nagai, M.A., da Silva, W. Jr., Zazo, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Balda, G.S., Simpson, D.H.,
Brunslein, A., de Oliveira, P.S., Bucher, P., Jonkeel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.P., Reis, J.F., de Souza, S.J., and
Simpson, A.J.

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Comment Contact: Simpson A.J.O.
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Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Genome Project.
This entry can be seen in the following URL
(http://www.ludwig.org.br/seq/gethtml.pl?1-QV612-QV-BT223-036.html
&13-220499614-1)

Features Seq primer: puc 18

Fax: +55 11 2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?1 MP15.2-MR1 C73529-140900-002-a125-2-2000-00-14874-1)
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 High quality sequence start: 2
 High quality sequence stop: 401.

FEATURES

Source
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 /db_xref="taxon:9606"
 /clone_lib="C10529"
 /dev_stage="Adult"
 /note="organ: colon; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORS15 PCR (9.S. letters patent application No. 196 716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 56 a 144 c 73 q 128 t
 ORIGIN

Alignment Scores:
 Pred. No.: 0.222 Length: 401
 Score: 69.00 Matches: 14
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DH: 14 Gaps: 0

US-09-856-070-17 (1-14) x Bg118349 (1-401)

QY 1 GluArqGluLysGluGlnMetMetArqGluLysGluGlnLeu 14
 |||||
 Db 285 CACACACAGAAATACACATCATCATCGCCGACAGACAGCAGCTTG 244

RESULT 15

BM/4471
 LOCUS BM744771 404 bp mRNA linear EST 01-MAR-2002
 DEFINITION K-EST0018496 SASNU1 Homo sapiens cDNA clone S4SNU1-18-D12 5', mRNA sequence.

ACCESSION BM744771

VERSION BM744771.1 GI:19066100

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 404)

Kim, N.S., Bahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.K., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.

21C Frontier Korean EST Project 2001

Unpublished (2002)

Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Eonam-dong Yusong-gu, Taejeon 305-333, South Korea

Tel.: +82-42-860-4470

Fax: +82-42-860-4409

Email: yonsung@mail.kribb.re.kr

Plate: 18 row: D column: 12

High quality sequence stop: 404.

Location/Qualifiers

1..404

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="S4SNU1-18-D12"

/clone_lib="S4SNU1"

/sex="M"

/tissue_type="Stomach"
 /cell_type="lymphoblast-like"
 /cell_line="SN0-1"
 /lab_host="top10f"

/note "Organ: Stomach, Vector: pTZ18KPI; Site_1: EcoRI; Site_2: NotI. The poly (A)⁺ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then dephosphated with tobacco acid pyrophosphatase (TAP). The dephosphated intact mRNA was ligated with DNA RNA linker including EcoRI 1 site. By treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10f⁺ by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

BASE COUNT 127 a 83 c 141 q 53 t
 ORIGIN

Alignment Scores:
 Pred. No.: 0.224 Length: 404
 Score: 69.00 Matches: 14
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DH: 14 Gaps: 0

US-09-856-070-17 (1-14) x BM744771 (1-404)

QY 1 GluArqGluLysGluGlnMetMetArqGluLysGluGlnLeu 14
 |||||
 Db 240 CACACACAGAAATACACATCATCATCGCCGACAGACAGCAGCTTG 281

Search completed: January 16, 2003, 21:37:02
 Job time : 1856.4 secs